

Figure 1 (SEQ ID NO:724)

## 85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG  
 AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA  
 GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC  
 TAAAGGTAAATAGAACTGCATTTCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC  
 TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA  
 GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179  
 gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12  
 gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12  
 emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds  
 Length = 1197

Score = 632 bits (319), Expect = e-179  
 Identities = 319/319 (100%)  
 Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 60  
 |||  
 Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaataagcta 120  
 |||  
 Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaataagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 180  
 |||  
 Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 834

Query: 181 aatcagcctaaaggtaaatagaaactgcatttcccctccattcttgaagccaatctttt 240  
 |||  
 Sbjct: 833 aatcagcctaaaggtaaatagaaactgcatttcccctccattcttgaagccaatctttt 774

Query: 241 caagaaatgactaagcagcacctgtgtgtgaagacagcaataaagcctgaacctgacact 300  
 |||  
 Sbjct: 773 caagaaatgactaagcagcacctgtgtgtgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319 (SEQ ID NO:725)  
 |||  
 Sbjct: 713 caagctttggtacaggatc 695 (SEQ ID NO:726)

Figure 2

cdNA Sequence and ORF of 85P1B3/OIP5 clone A  
(SEQ ID NO:727)

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      9      18      27      36      45      54
5' GGC TGC GGG AAG ATG GCG GCT CAG CCG CTG CGG CAT CGC TCA CGT TGT GCA ACG
   (SEQ ID NO:728)→ M  A  A  Q  P  L  R  H  R  S  R  C  A  T

      63      72      81      90      99     108
CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT
   P  P  R  G  D  F  C  G  G  T  E  R  A  I  D  Q  A  S

      117     126     135     144     153     162
TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG GGG TCC TCG CCG CTC
   F  T  T  S  M  E  W  D  T  Q  V  V  K  G  S  S  P  L

      171     180     189     198     207     216
GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT
   G  P  A  G  L  G  A  E  E  P  A  A  G  P  Q  L  P  S

      225     234     243     252     261     270
TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG
   W  L  Q  P  E  R  C  A  V  F  Q  C  A  Q  C  H  A  V

      279     288     297     306     315     324
CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG
   L  A  D  S  V  H  L  A  W  D  L  S  R  S  L  G  A  V

      333     342     351     360     369     378
GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC
   V  F  S  R  V  T  N  N  V  V  L  E  A  P  F  L  V  G

      387     396     405     414     423     432
ATT GAA GGT TCA CTC AAA GGC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT
   I  E  G  S  L  K  G  S  T  Y  N  L  L  F  C  G  S  C

      441     450     459     468     477     486
GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GCC CTG GCT GCC TTG
   G  I  P  V  G  F  H  L  Y  S  T  H  A  A  L  A  A  L

      495     504     513     522     531     540
AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA
   R  G  H  F  C  L  S  S  D  K  M  V  C  Y  L  L  K  T

      549     558     567     576     585     594
AAA GCC ATA GTA AAT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA
   K  A  I  V  N  A  S  E  M  D  I  Q  N  V  P  L  S  E

      603     612     621     630     639     648
AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA
   K  I  A  E  L  K  E  K  I  V  L  T  H  N  R  L  K  S

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657				666				675				684				693				702	
CTA	ATG	AAG	ATT	CTG	AGT	GAA	GTG	ACT	CCT	GAC	CAG	TCC	AAG	CCA	GAA	AAC	TGA				
L	M	K	I	L	S	E	V	T	P	D	Q	S	K	P	E	N	*				
711				720				729				738				747				756	
TCC	TGT	ACC	AAA	GCT	TGA	GTG	TCA	GGT	TCA	GGC	TTT	ATT	GCT	GTC	TTC	AAC	AAC				
765				774				783				792				801				810	
AGG	TGC	TGC	TTA	GTC	ATT	TCT	TGA	AAA	AGA	TTG	GCT	TCA	AGA	ATG	GAG	GGG	AAA				
819				828				837				846				855				864	
TGC	AGT	TTC	TAT	TTA	CCT	TTA	GGC	TGA	TTT	TCC	AAA	TTA	TTT	GTG	AAG	CTG	TTT				
873				882				891				900				909				918	
TTA	GAA	GAT	GAG	AGA	CTA	AGG	ATT	CTT	CTC	TTT	TAT	AGC	TAT	TTG	CCT	TAA	GAA				
927				936				945				954				963				972	
CTT	ACT	TTA	GAT	TCT	TAT	TGA	ATT	CAT	AAT	ACT	TAT	CTC	TGA	AAA	TGT	CTT	TGA				
981				990				999				1008				1017				1026	
CTG	TAA	ATT	TAG	GAA	TTA	AGA	TGC	AGA	GTC	CCA	TGT	GTC	CTC	TGA	TCT	AAA	GTT				
1035				1044				1053				1062				1071				1080	
GCA	TGG	TTG	GTC	TGA	AAA	TAG	AGT	TGG	GCT	TAA	TGT	TGA	CTT	CTA	TTA	CTC	CTG				
1089				1098				1107				1116				1125				1134	
CAT	GGA	GCA	GTT	GTT	ATG	AAT	ACT	AAT	ACA	TCA	CTT	TTT	AAC	TTC	TGT	AAA	ATA				
1143				1152				1161				1170				1179				1188	
CAG	ATC	ATA	ATA	TTC	TAT	AGG	TAA	TGT	TTA	ATA	AAT	TGC	CTG	AAT	AAT	AAA	AAA				
1197				1206				1215				1224				1233				1242	
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA				
1251				1260																	
AAA AAA AAA AAA AAA AAA AA 3'																					

Figure 3

85P1B3/OIP5 protein sequence. (SEQ ID NO:729)

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1  MAAQPLRHRS RCATPPRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGSSPL GPAGLGAEED
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHAWDLRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*
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Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1|(AF025441) Opa-interacting protein OIP5 [Homo sapiens]  
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

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85P1B3: 1  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEAP 60
            MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEAP
OIP5: 3      MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEAP 62

85P1B3: 61  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL 120
            AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL
OIP5: 63     AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL 122

85P1B3:121  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
            VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
OIP5: 123    VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 182

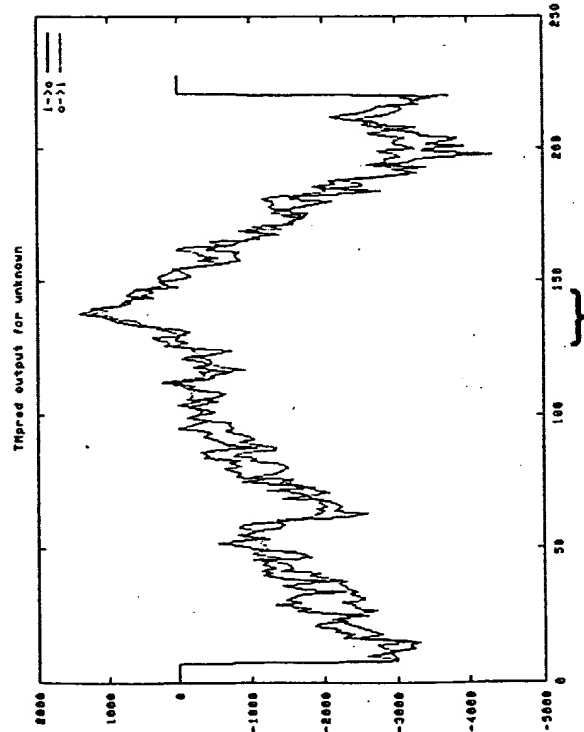
85P1B3:181  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229 (SEQ ID NO:730)
            NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
OIP5: 183    NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 231 (SEQ ID NO:731)

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Fig. 21A

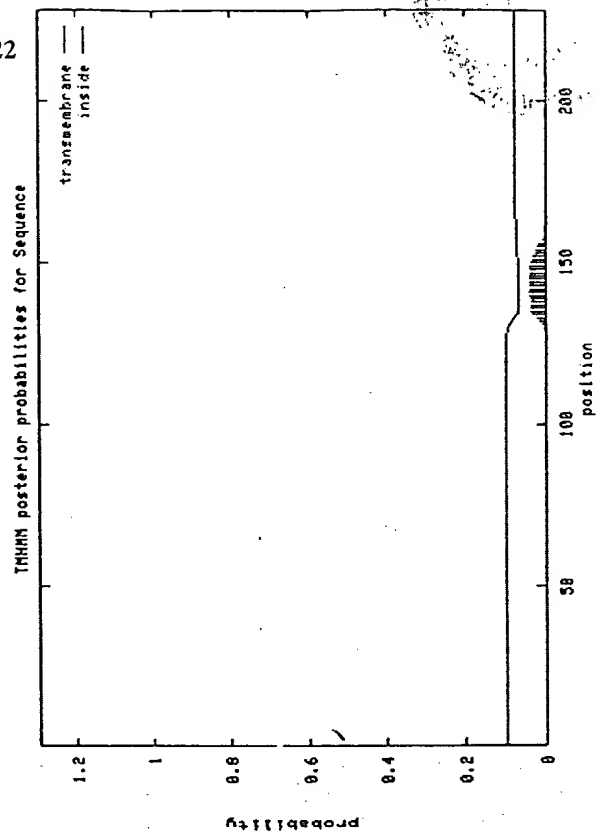
MAAQPLRHRRCATPPRGDFCGGTERAIDQASFTTSMEDTQVVKSSPLGPAGLGAEEPAAGPQLPSWL  
 c: random coil (49.34%)  
 ccc  
 e: extended strand (13.97%)  
 QPERCAVFQCAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVLEAPFLVGIEGSLKGSTYNLLFCGSC  
 h: alpha helix (36.68%)  
 chhh  
 GIPVGFHLYSTHAALALRGHFCLSDDKMCVYLLKTKAIVNASMDIQNVPLSEKIAELKEKIVLTHNRL  
 cccchhh  
 KSLMKILSEVTPDQSKPEN (SEQ ID NO:729)  
 hhhhhhecccccccccccc

Fig. 21B



1 transmembrane from amino acids 129-149

Fig. 21C



No transmembrane domains, soluble protein